

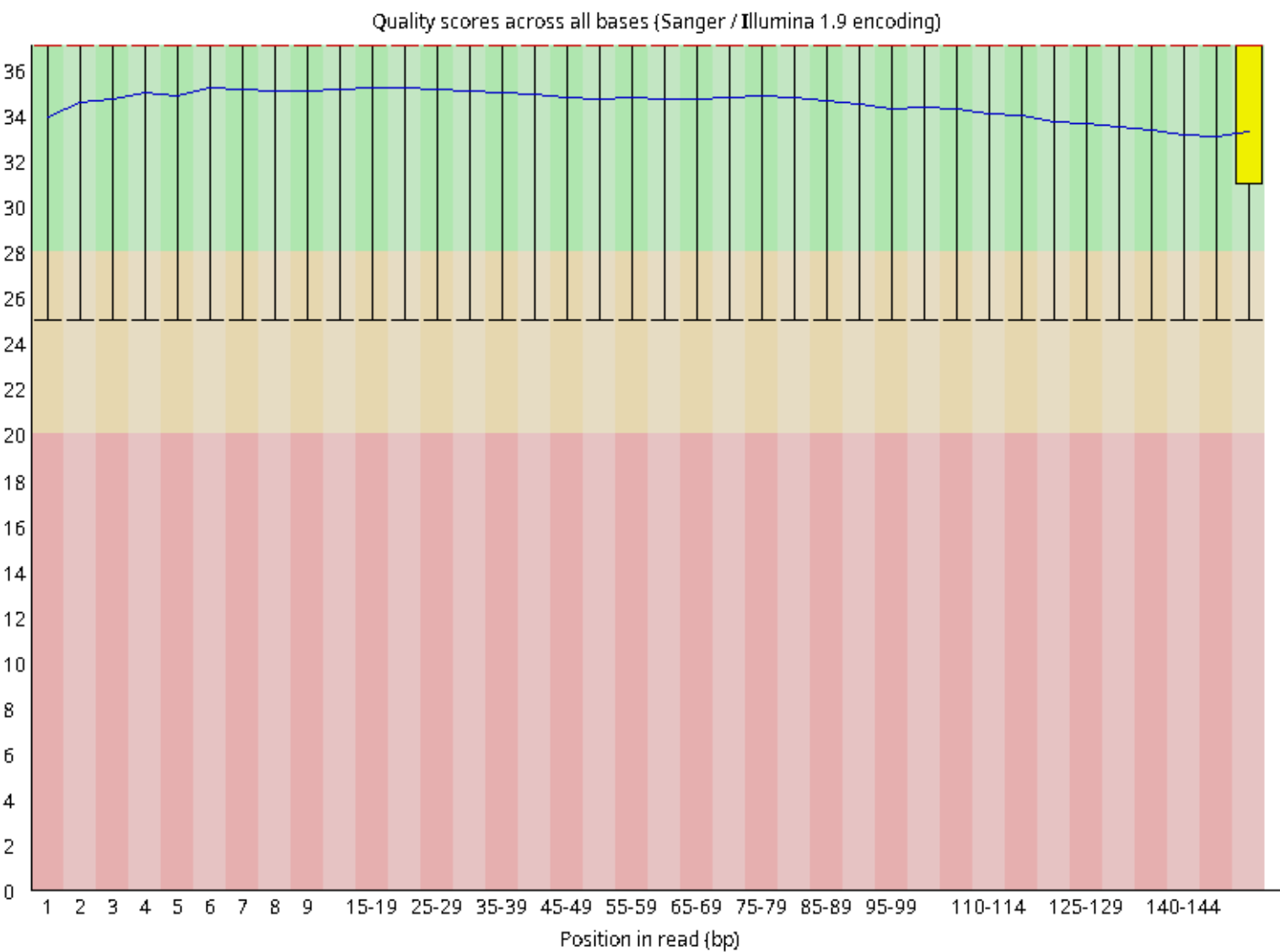
Summary

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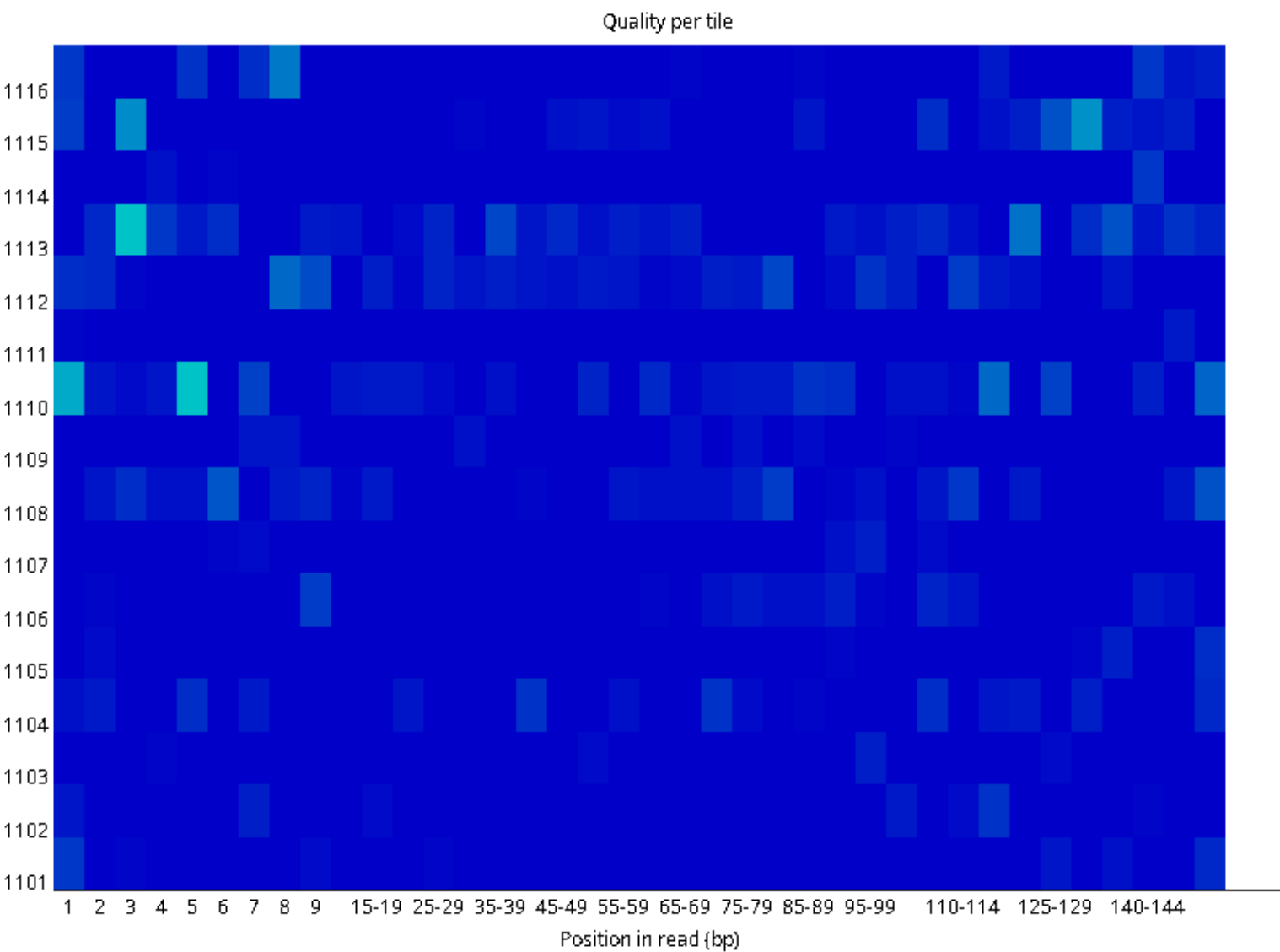
✓ Basic Statistics

Measure	Value
Filename	SRR33784444_2_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	6696
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	46

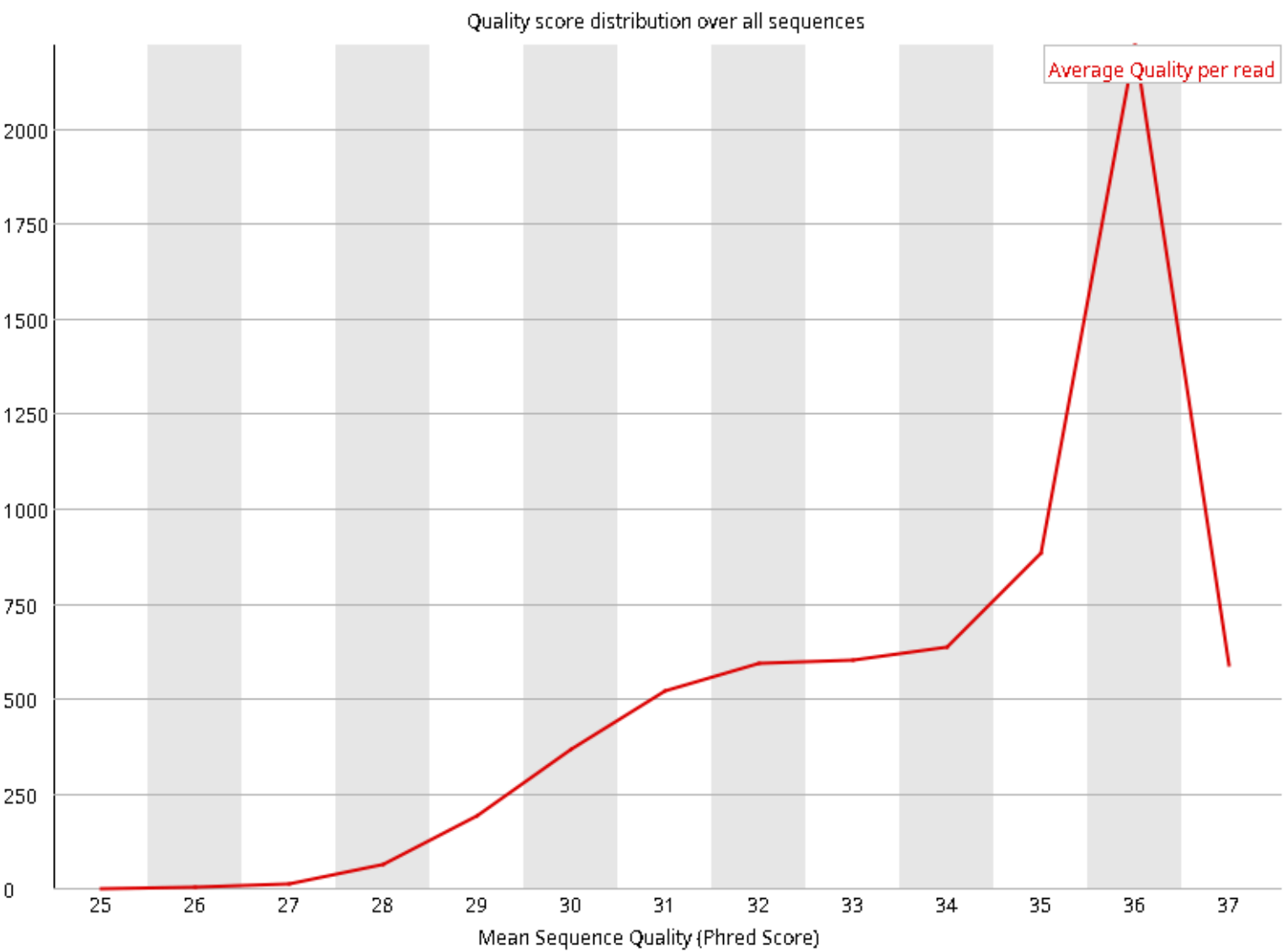
✔ Per base sequence quality



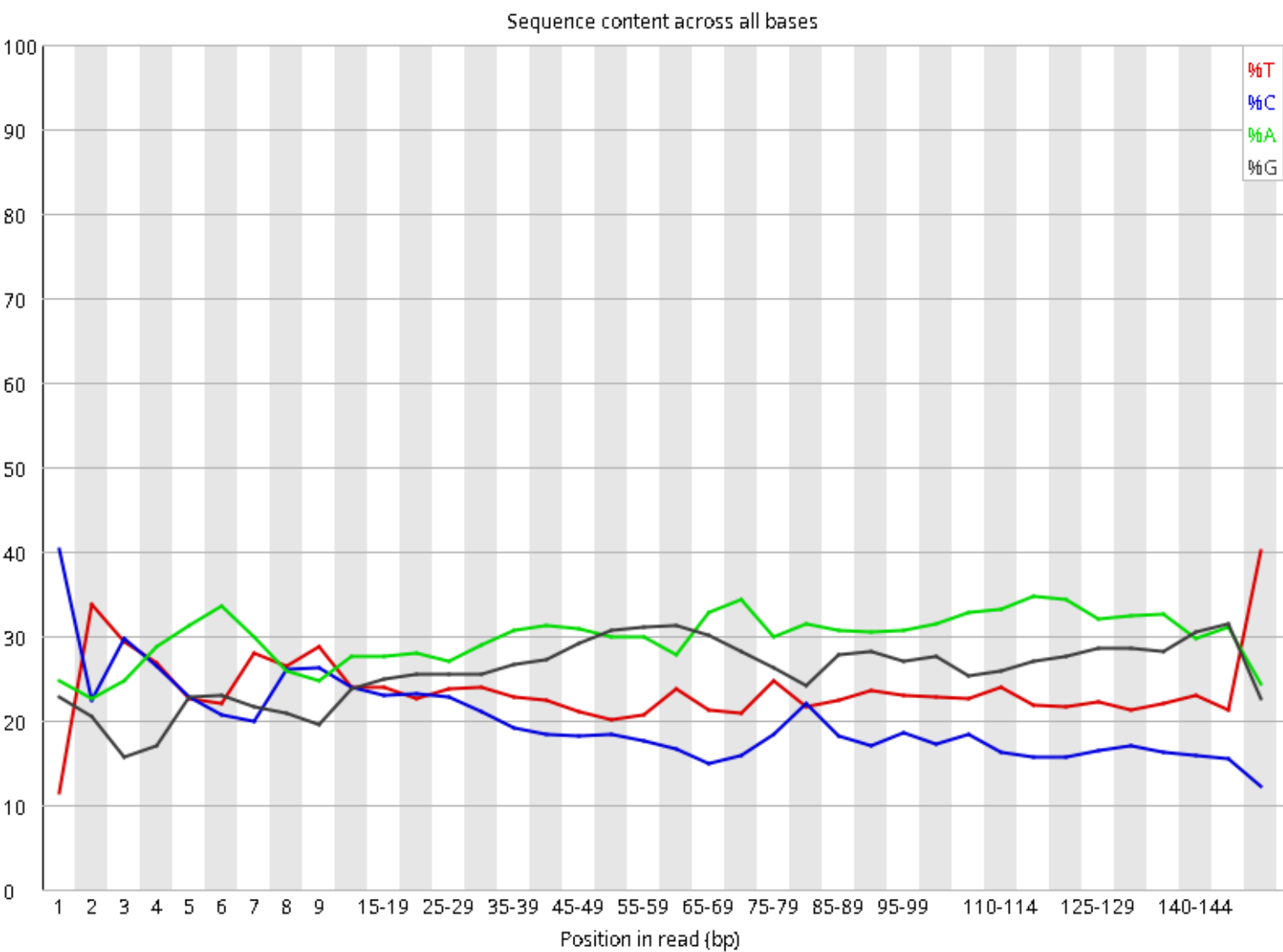
Per tile sequence quality



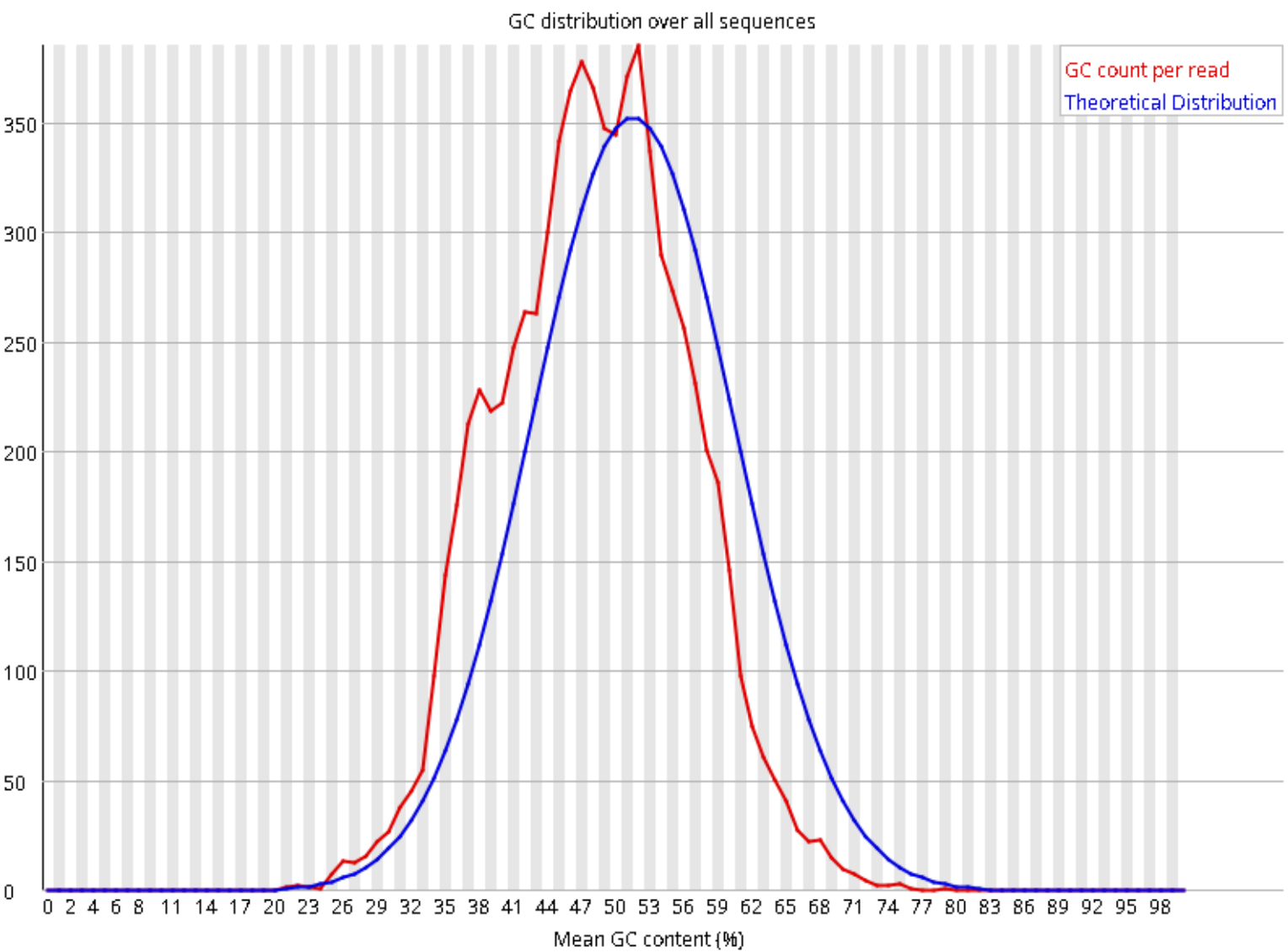
Per sequence quality scores



! Per base sequence content

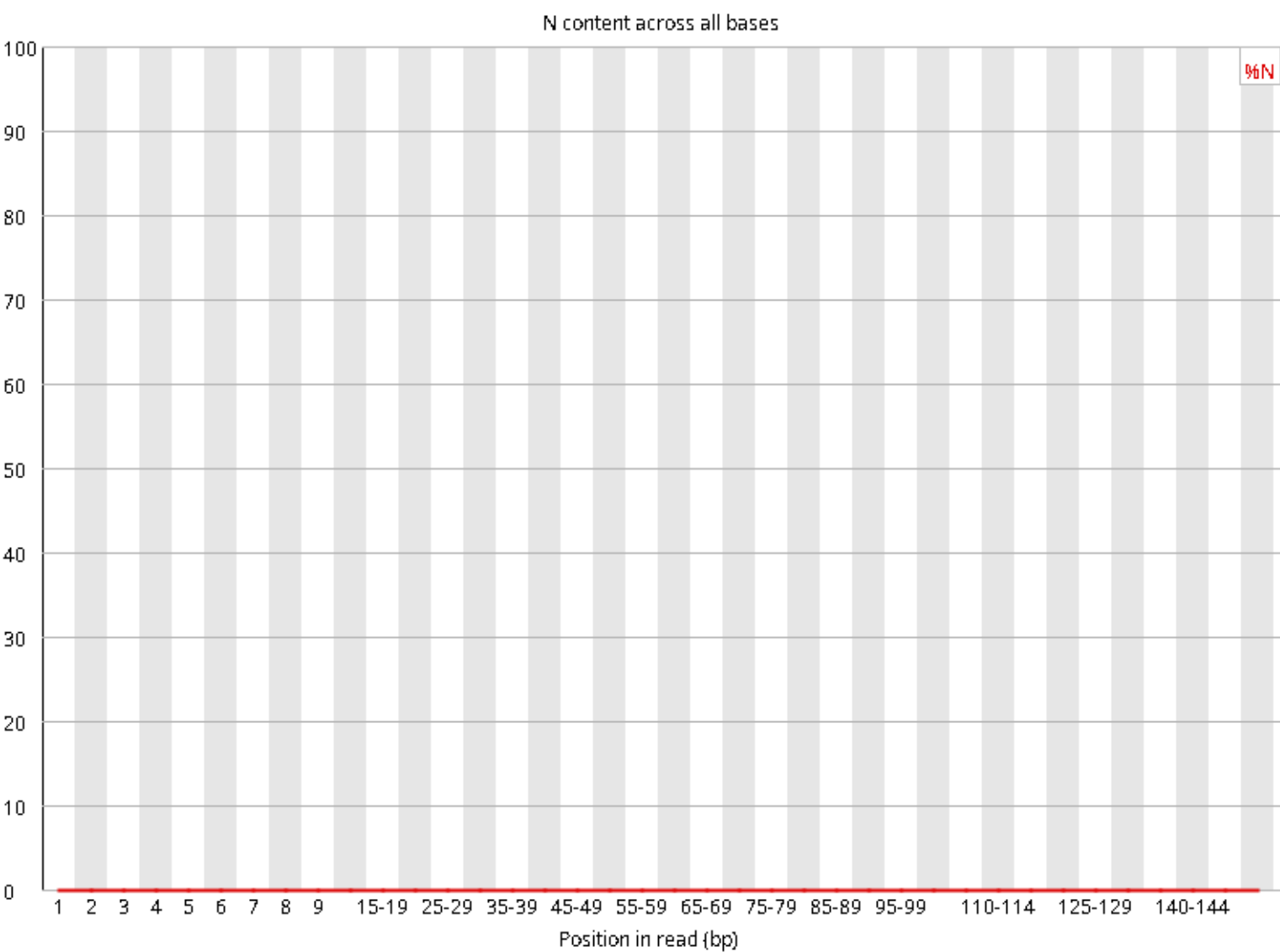


✖ Per sequence GC content

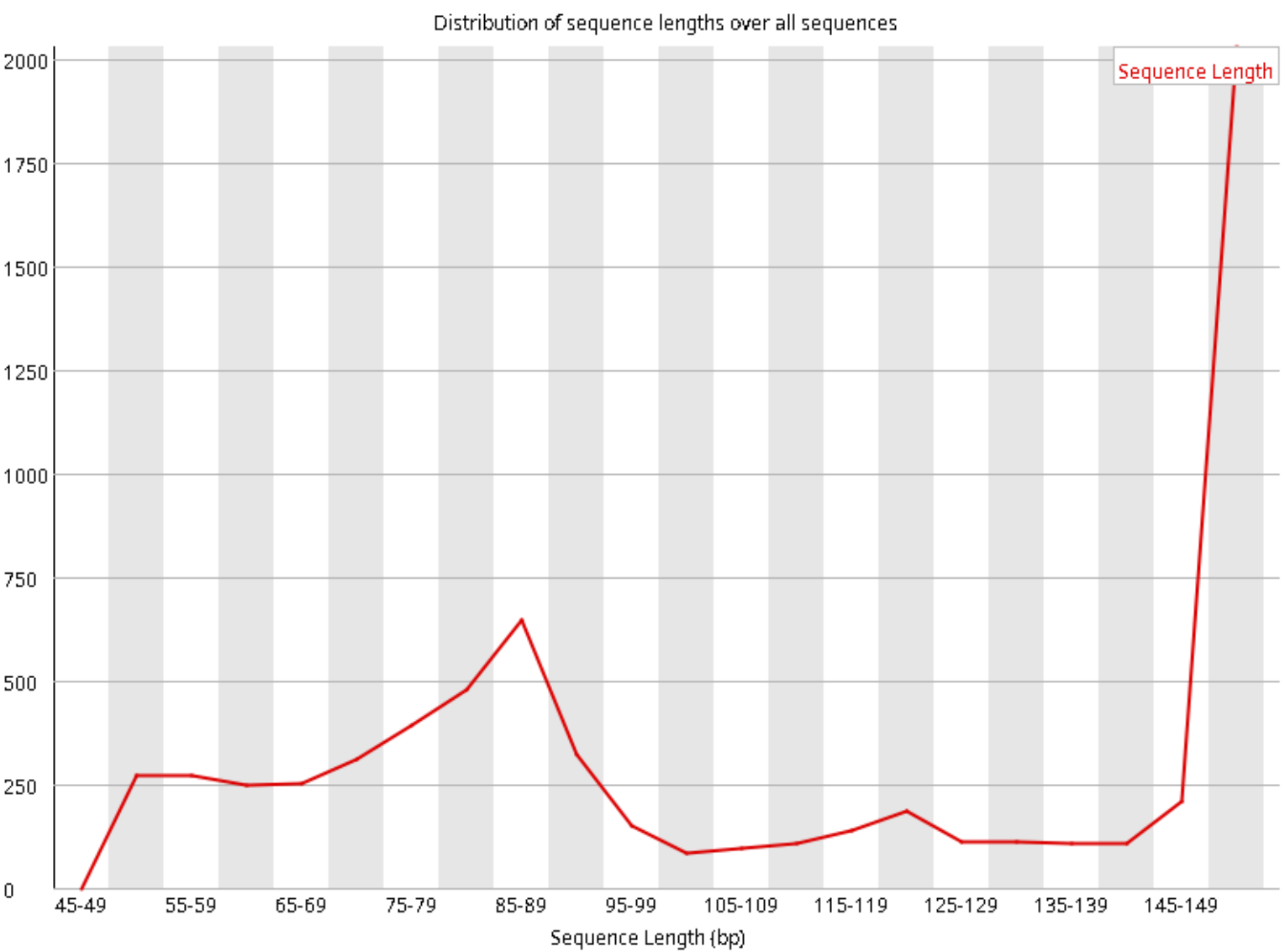




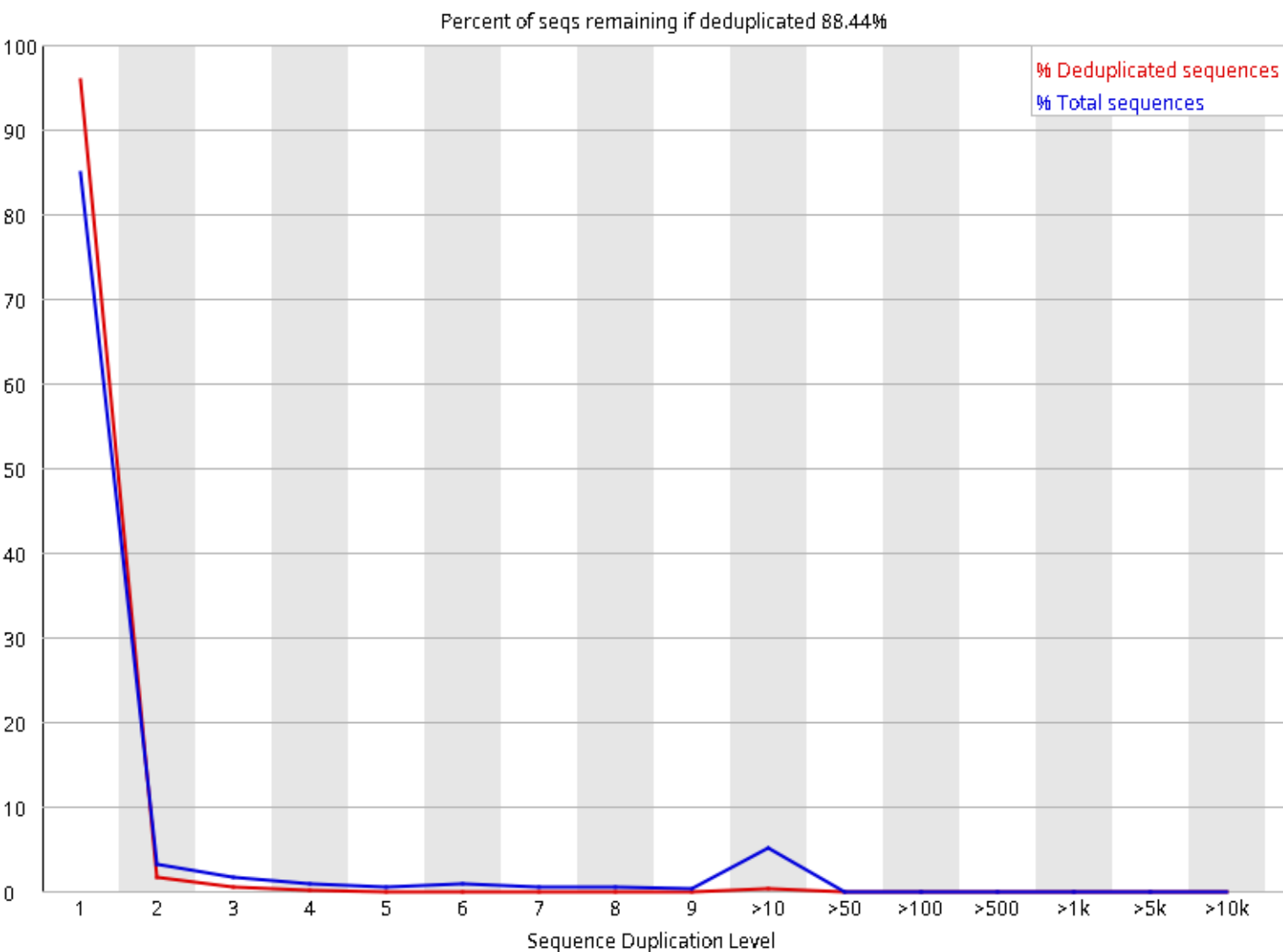
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



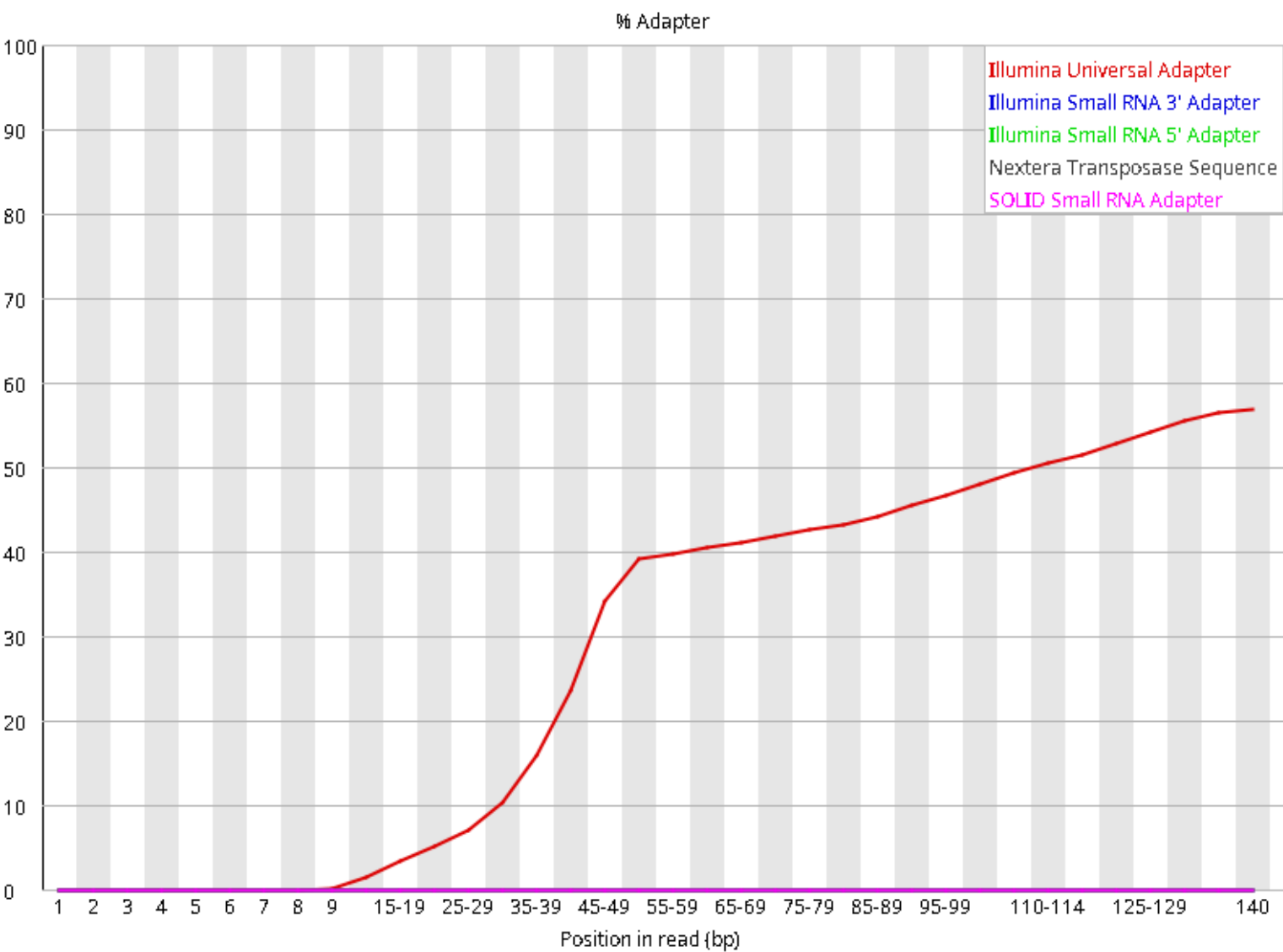
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGACAGCTAATA	26	0.38829151732377537	No Hit
CCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGG	25	0.37335722819593786	No Hit
CCCCTAGTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGA	22	0.32855436081242534	No Hit
CCTTGTACAAGGAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTACACGCAGT	20	0.2986857825567503	Illumina Single End PCR Primer 1 (96% over 33bp)
CACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGGAG	20	0.2986857825567503	No Hit
CTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATTAGAACA	18	0.2688172043010753	No Hit
CTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGA	18	0.2688172043010753	No Hit

Sequence	Count	Percentage	Possible Source
CTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGACAGCTAATAGA	17	0.25388291517323774	No Hit
AGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGGAGCAG	17	0.25388291517323774	No Hit
CCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAG	16	0.23894862604540024	No Hit
CCCTAGTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGAC	15	0.2240143369175627	No Hit
CCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGG	15	0.2240143369175627	No Hit
CTCTATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAAATTTA	14	0.2090800477897252	No Hit
GTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGG	13	0.19414575866188769	No Hit
GCTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATTAGAAC	13	0.19414575866188769	No Hit
AGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAA	13	0.19414575866188769	No Hit
CCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTA	12	0.17921146953405018	No Hit
GGGACAGCTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTAT	11	0.16427718040621267	No Hit
CTATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAAATTTACC	11	0.16427718040621267	No Hit
CACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGACAGCTAA	11	0.16427718040621267	No Hit
CAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGGAGCA	10	0.14934289127837516	No Hit
ATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAAATTTACCAG	10	0.14934289127837516	No Hit
CCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAA	10	0.14934289127837516	No Hit
CCTTGTACAAGGAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTACACGCAG	9	0.13440860215053765	Illumina Single End PCR Primer 1 (96% over 33bp)
CTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGG	9	0.13440860215053765	No Hit
CTCTCAGAGAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTACACGCAGT	9	0.13440860215053765	Illumina Single End PCR Primer 1 (96% over 33bp)
ATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGACAGCT	8	0.11947431302270012	No Hit
GTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGGAGCAGA	8	0.11947431302270012	No Hit
TACCACCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCA	8	0.11947431302270012	No Hit
GTTACCACCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGT	8	0.11947431302270012	No Hit
AGAAGGGAGAAGAGTTACCACCCTTAACCTCCCTCAAATCACTCTTTGGC	8	0.11947431302270012	No Hit
CCACCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACA	7	0.1045400238948626	No Hit
ACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATA	7	0.1045400238948626	No Hit
CCTAGTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACA	7	0.1045400238948626	No Hit
GGGGACAGCTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTA	7	0.1045400238948626	No Hit
GGACAGCTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATT	7	0.1045400238948626	No Hit
AGTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAG	7	0.1045400238948626	No Hit
CCTGAAGCAGGAGCAGAAGGGAGAAGAGTTACCACCCTTAACCTCCCTCA	7	0.1045400238948626	No Hit



Adapter Content



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